

## SEQUENCE LISTING

<110> Saucier, Caroline  
Park, Morag  
Pawson, Anthony J.  
Lai, Ka-Man

<120> SHC MODULATION AND USES THEREOF

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<151> 2003-02-19

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Arg 210	Lys	Pro	Cys	Ser	Arg	Pro 215	Leu	Ser	Ser	Ile	Leu 220	Gly	Arg	Ser	Asn
Leu 225	Lys	Phe	Ala	Gly	Met 230	Pro	Ile	Thr	Leu	Thr 235	Val	Ser	Thr	Ser	Ser 240
Leu	Asn	Leu	Met	Ala 245	Ala	Asp	Cys	Lys	Gln 250	Ile	Ile	Ala	Asn	His 255	His
Met	Gln	Ser	Ile 260	Ser	Phe	Ala	Ser	Gly 265	Gly	Asp	Pro	Asp	Thr 270	Ala	Glu
Tyr	Val	Ala 275	Tyr	Val	Ala	Lys	Asp 280	Pro	Val	Asn	Gln	Arg 285	Ala	Cys	His
Ile	Leu	Glu	Cys	Pro	Glu	Gly	Leu	Ala	Gln	Asp	Val	Ile	Ser	Thr	Ile

290		295		300
Gly 305	Gln 310	Ala 315	Phe 320	Glu 325
Leu 330	Arg 335	Phe 340	Lys 345	Gln 350
Tyr 355	Leu 360	Arg 365	Asn 370	Pro 375
Pro 380				
Lys 385	Leu 390	Val 395	Thr 400	Pro 405
His 410	Asp 415	Arg 420	Met 425	Ala 430
Gly 435	Phe 440	Asp 445	Gly 450	Ser 455
Trp 460	Asp 465	Glu 470	Glu 475	Glu 480
Pro 485	Pro 490	Pro 495	His 500	Gln 505
Ala 510	Gly 515	Val 520	Asn 525	Gly 530
Leu 535	Val 540	Arg 545	Pro 550	Pro 555
Phe 560	Val 565	Asp 570	Met 575	Arg 580
Leu 585	Arg 590	Pro 595	Asn 600	Pro 605
Val 610	Gln 615	Val 620	Asn 625	Pro 630
Ala 635	Pro 640	Thr 645	Pro 650	Arg 655
Ala 660	Pro 665	Thr 670	Pro 675	Arg 680
Ala 685	Pro 690	Thr 695	Pro 700	Arg 705
Ala 710	Pro 715	Thr 720	Pro 725	Arg 730
Ala 735	Pro 740	Thr 745	Pro 750	Arg 755
Ala 760	Pro 765	Thr 770	Pro 775	Arg 780
Ala 785	Pro 790	Thr 795	Pro 800	Arg 805
Ala 810	Pro 815	Thr 820	Pro 825	Arg 830
Ala 835	Pro 840	Thr 845	Pro 850	Arg 855
Ala 860	Pro 865	Thr 870	Pro 875	Arg 880
Ala 885	Pro 890	Thr 895	Pro 900	Arg 905
Ala 910	Pro 915	Thr 920	Pro 925	Arg 930
Ala 935	Pro 940	Thr 945	Pro 950	Arg 955
Ala 960	Pro 965	Thr 970	Pro 975	Arg 980
Ala 985	Pro 990	Thr 995	Pro 1000	Arg 1005

530

535

540

Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met  
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Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln  
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Gln Pro Val Glu Arg Lys Leu  
 580

<210> 7

<211> 1462

<212> DNA

<213> Mus musculus

<400> 7

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gtggaccaga cacgggagct ttgtcaataa gcccacacga ggctggctgc atcccaacga  
 180

caaagtcattg ggacctgggg tttctacttt ggttcggtac atgggctgtg tggaggtctt  
 240

acagtcaatg cgagcccttg acttcaatac ccggactcag gtcaccaggg aggccatcag  
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tttggtgtgt gaagctgtgc ctggtgccaa aggggcgaca aggaggagaa agccttgtag  
 360

ccgcccactc agtccatcc tggggaggag taacctgaag ttgctggaa tgccaatcac  
 420

tctcactgtg tctaccagca gccttaacct catggcagcc gactgcaaac agatcattgc  
 480

caaccatcac atgcaatcta tctctttcgc gtccgggtggg gatccggaca cagctgagta  
 540

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tgaagggtct gctcaggatg tcatcagcac catcgggcag gcctttgagt tgcgcttcaa  
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1080

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1140

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1200

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1260

tggccagtat gtgctcactg gcctgcagag tgggcagccc aagcacttgc tgctggtgga  
1320

ccctgaaggt gtggttcgga caaaggatca ccgctttgag agtgtcagtc acctgatcag  
1380

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<210> 8

<211> 469

<212> PRT

<213> Mus musculus

<400> 8

Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly  
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Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn  
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Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro  
35 40 45

Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln  
50 55 60

Ser	Met	Arg	Ala	Leu	Asp	Phe	Asn		Thr	Arg	Thr	Gln	Val	Thr	Arg	Glu
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Ala	Ile	Ser	Leu	Val	Cys	Glu	Ala	Val	Pro	Gly	Ala	Lys	Gly	Ala	Thr	
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Arg	Arg	Arg	Lys	Pro	Cys	Ser	Arg	Pro	Leu	Ser	Ser	Ile	Leu	Gly	Arg	
			100					105					110			
Ser	Asn	Leu	Lys	Phe	Ala	Gly	Met	Pro	Ile	Thr	Leu	Thr	Val	Ser	Thr	
		115					120					125				
Ser	Ser	Leu	Asn	Leu	Met	Ala	Ala	Asp	Cys	Lys	Gln	Ile	Ile	Ala	Asn	
		130				135					140					
His	His	Met	Gln	Ser	Ile	Ser	Phe	Ala	Ser	Gly	Gly	Asp	Pro	Asp	Thr	
145					150					155					160	
Ala	Glu	Tyr	Val	Ala	Tyr	Val	Ala	Lys	Asp	Pro	Val	Asn	Gln	Arg	Ala	
				165					170					175		
Cys	His	Ile	Leu	Glu	Cys	Pro	Glu	Gly	Leu	Ala	Gln	Asp	Val	Ile	Ser	
			180					185					190			
Thr	Ile	Gly	Gln	Ala	Phe	Glu	Leu	Arg	Phe	Lys	Gln	Tyr	Leu	Arg	Asn	
		195					200					205				
Pro	Pro	Lys	Leu	Val	Thr	Pro	His	Asp	Arg	Met	Ala	Gly	Phe	Asp	Gly	
		210				215					220					
Ser	Ala	Trp	Asp	Glu	Glu	Glu	Glu	Glu	Pro	Pro	Asp	His	Gln	Tyr	Tyr	
225					230					235					240	
Asn	Asp	Phe	Pro	Gly	Lys	Glu	Pro	Pro	Leu	Gly	Gly	Val	Val	Asp	Met	
				245					250					255		
Arg	Leu	Arg	Glu	Gly	Ala	Ala	Arg	Pro	Thr	Leu	Pro	Ser	Ala	Gln	Met	
			260					265					270			
Ser	Ser	His	Leu	Gly	Ala	Thr	Leu	Pro	Ile	Gly	Gln	His	Ala	Ala	Gly	
		275					280					285				
Asp	His	Glu	Val	Arg	Lys	Gln	Met	Leu	Pro	Pro	Pro	Pro	Cys	Pro	Gly	
		290				295					300					

Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Ile Gln Asn Leu Asp  
 305 310 315 320

Lys Ala Arg Gln Ala Gly Gly Gly Ala Gly Pro Pro Asn Pro Ser Leu  
 325 330 335

Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe Glu Asp  
 340 345 350

Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Met Ser Met Ala Glu Gln  
 355 360 365

Leu Gln Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg Glu Ala  
 370 375 380

Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu Ser Thr  
 385 390 395 400

Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly Gln Pro  
 405 410 415

Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr Lys Asp  
 420 425 430

His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met Asp Asn  
 435 440 445

His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln Gln Pro  
 450 455 460

Val Asp Arg Lys Val  
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<210> 9

<211> 1739

<212> DNA

<213> Mus musculus

<400> 9

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ttctttcccc ggatgagcaa cctgaagctg gccaatcctg ctggggggcg cctggggcct  
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aaaggggagc caggaaaggc tgctgaagat ggggaaggga gtgcaggggc agcccttcgg  
300

gactcaggcc tcttgccct cctccaggac atgaacaagc tgagtggagg cggcggggcg  
360

aggactcggg tagaaggggg ccagctgggg ggcgaggagt ggaccagaca cgggagcttt  
420

gtcaataagc ccacacgagg ctggctgcat cccaacgaca aagtcatggg acctgggggt  
480

tcctacttgg ttcggtacat gggctgtgtg gaggtcttac agtcaatgcg agcccttgac  
540

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ggtgccaaag gggcgacaag gaggagaaag ccttgtagcc gccactcag ctccatcctg  
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gggaggagta acctgaagtt tgctggaatg ccaatcactc tactgtgtc taccagcagc  
720

cttaacctca tggcagccga ctgcaaacag atcattgcc accatcacat gcaatctatc  
780

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840

cctgtgaatc agagagcctg ccatatcctg gagtgtcctg aagggttgc tcaggatgtc  
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960

aagctgggtca ccccccata caggatggct ggctttgatg gctcagcttg ggatgaggag  
1020

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1080

ggtgggggtg tagatatgag gcttcgggaa ggggctgctc gaccactct gcctagtgc  
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1200

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1260

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1380

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1440

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1560

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1620

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<210> 10

<211> 579

<212> PRT

<213> Mus musculus

<400> 10

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu  
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Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro  
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg  
50 55 60

Met Ser Asn Leu Lys Leu Ala Asn Pro Ala Gly Gly Arg Leu Gly Pro  
65 70 75 80

Lys Gly Glu Pro Gly Lys Ala Ala Glu Asp Gly Glu Gly Ser Ala Gly  
85 90 95

Ala Ala Leu Arg Asp Ser Gly Leu Leu Pro Leu Leu Gln Asp Met Asn  
100 105 110

Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln  
115 120 125

Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro  
130 135 140

Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val  
145 150 155 160

Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met  
165 170 175

Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile  
180 185 190

Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg  
195 200 205

Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn  
210 215 220

Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser  
225 230 235 240

Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His  
245 250 255

Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu  
260 265 270

Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His  
275 280 285

Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile  
290 295 300

Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro  
305 310 315 320

Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala  
325 330 335

Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp  
340 345 350

Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu  
355 360 365

Arg Glu Gly Ala Ala Arg Pro Thr Leu Pro Ser Ala Gln Met Ser Ser  
370 375 380

His Leu Gly Ala Thr Leu Pro Ile Gly Gln His Ala Ala Gly Asp His  
 385 390 395 400

Glu Val Arg Lys Gln Met Leu Pro Pro Pro Pro Cys Pro Gly Arg Glu  
 405 410 415

Leu Phe Asp Asp Pro Ser Tyr Val Asn Ile Gln Asn Leu Asp Lys Ala  
 420 425 430

Arg Gln Ala Gly Gly Gly Ala Gly Pro Pro Asn Pro Ser Leu Asn Gly  
 435 440 445

Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe Glu Asp Ala Leu  
 450 455 460

Arg Val Pro Pro Pro Pro Gln Ser Met Ser Met Ala Glu Gln Leu Gln  
 465 470 475 480

Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg Glu Ala Glu Ala  
 485 490 495

Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu Ser Thr Thr Thr  
 500 505 510

Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly Gln Pro Lys His  
 515 520 525

Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr Lys Asp His Arg  
 530 535 540

Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met Asp Asn His Leu  
 545 550 555 560

Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln Gln Pro Val Asp  
 565 570 575

Arg Lys Val

<210> 11  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence  
 <220>

<223> RTK binding site variant

<400> 11

Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val  
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<210> 12

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 12

Leu Pro Val Pro Glu Phe Ile Asn Gln Ser Val  
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<210> 13

<211> 11

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<223> RTK binding site variant

<400> 13

Ile Glu Asn Pro Gln Tyr Phe Ser Asp Ala Cys  
1 5 10

<210> 14

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> RTK binding site variant

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Ile Glu Asn Pro Gln Phe Phe Ser Asp Ala Cys  
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<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 15



Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro  
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<210> 16  
<211> 9  
<212> PRT  
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<220>  
<223> RTK variants

<400> 16

Asn Ala Thr Phe Val Asn Val Lys Cys  
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